

Raw Sequence Listing Error Summary

01P2

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 101051,644A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply
Corrective Action Needed

OIPE

RAW SEQUENCE LISTING

DATE: 12/09/2002

PATENT APPLICATION: US/10/051,644A

TIME: 12:55:28

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

3 <110> APPLICANT: Liu, et al.
 5 <120> TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
 6 Parasitic Nematodes
 8 <130> FILE REFERENCE: 2002630-0012
 10 <140> CURRENT APPLICATION NUMBER: 10/051,644A
 C--> 11 <141> CURRENT FILING DATE: 2002-11-19

13 <160> NUMBER OF SEQ ID NOS: 8

15 <170> SOFTWARE: PatentIn Ver. 2.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 425

19 <212> TYPE: PRT

20 <213> ORGANISM: Artificial Sequence

22 <220> FEATURE:

23 <223> OTHER INFORMATION: Description of Artificial Sequence

24 Sequence

26 <400> SEQUENCE: 1

27 Met Ala Val Leu Ala Val Val Leu Leu Ala Cys Leu Glu Arg Ala

28 1 5 10 15

30 Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala

31 20 25 30

33 Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala

34 35 40 45

36 Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn

37 50 55 60

39 Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu

40 65 70 75 80

42 Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp

43 85 90 95

45 Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro

46 100 105 110

48 Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val

49 115 120 125

51 Gly Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg

52 130 135 140

54 Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr

55 145 150 155 160

57 Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile

58 165 170 175

60 Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr

61 180 185 190

63 Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly

64 195 200 205

66 Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.



Amino Acid

must explain genetic source
 see error summary
 sheet item 11

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DATE: 12/09/2002

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Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

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69 Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu
70 225      230      235      240
72 Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala
73      245      250      255
75 Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro
76      260      265      270
78 Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp
79      275      280      285
81 Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly
82      290      295      300
84 Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile
85 305      310      315      320
87 Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp
88      325      330      335
90 Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg
91      340      345      350
93 Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile
94      355      360      365
96 Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln
97      370      375      380
99 Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly
100 385      390      395      400
102 Ser Pro Cys Thr Ala Asp Ala Asp Cys Pro Gly Thr Gln Thr Cys Ser
103      405      410      415
105 Val Ala Glu Ala Leu Cys Val Ile Pro
106      420      425
109 <210> SEQ ID NO: 2
110 <211> LENGTH: 1341
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA Nucleotide
116      Sequence
118 <400> SEQUENCE: 2
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120 ttcggctgct ctaacaccaa gatcaatgac caggctcgta agatgttcta tgatgctcac 120
121 aatgatgcaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180
122 ggtggaaaga atgtttatga attgaattgg gattgcgaga tggaagcaaa agctcaggaa 240
123 tgggcagacg gatgtcccag ctctttccag acatttgatc caacatgggg gcagaactac 300
124 gcgacgtaca tgggatcgat tgctgatccg cttccatacg cttccatggc tgtaaatggg 360
125 tggtggtcgg aaattagaac cgtaggactt acggatcctg ataacaagta cactaacagt 420
126 gcaatgttcc gatttgctaa tatggcaaat ggtaaagctt cagcttttgg atgtgcatac 480
127 gcgttggtcg caggaaaact atccatcaat tgcatttaca acaagatagg atacatgacc 540
128 aatgctatca tttatgaaaa aggagatgcc tgtaccagtg acgctgaatg caccacctac 600
129 tcagactcac aatgcaaaaa cggctcttgc tataaggcac ctcaagctcc agtcgttgag 660
130 actttcacia tgtgcccttc ggtcacggac cagtcggatc aggcgcgtca aaacttcttg 720
131 gacacccata acaaattgcg tacaagcctt gccaaaggac ttgaagctga tgggaattgcc 780
132 gctggagcat ttgcaccaat ggccaagcaa atgccaaaac tggtaaaata cagctgcaca 840

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Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

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133 gttgaagcaa acgccagaac atgggcaaaa ggatgccttt accagcattc aacaagcgca 900
134 cagagaccag gactcgggtga aaatctttat atgatcagca ttaacaacat gcctaaaatt 960
135 caaaccgcgg aggactcctc aaaggcttgg tgggccgagt tgaagactt cggagtcggt 1020
136 tctgacaaca ttctgaccca agcagttttt gatcgtggcg ttggacatta cacacaaatg 1080
137 gcatgggaag gaactactga aattggatgt tttgtggaga attgtccaac attcacttat 1140
138 tccgtatgcc aatatggtcc agcgggaaac tacatgaacc aactaatcta taccaagggc 1200
139 tcaccatgca cagctgacgc cgattgcccc ggaaccgaga catgcagtgt cgctgaagca 1260
140 ttatgtgta tcccttagta aattttctat gcaactcttt gaaagtcata ataaatatgc 1320
141 aaaaattaaa aaaaaaaaaa a                                     1341

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144 <210> SEQ ID NO: 3

145 <211> LENGTH: 473

146 <212> TYPE: PRT

147 <213> ORGANISM: Artificial Sequence

149 <220> FEATURE:

150 <223> OTHER INFORMATION: Description of Artificial Sequence (Amino Acid

151 Sequence)

153 <400> SEQUENCE: 3

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158           20           25           30
160 Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu
161           35           40           45
163 Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser
164   50           55           60
166 Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu
167  65           70           75           80
169 Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu
170           85           90           95
172 Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu
173           100          105          110
175 Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met
176           115          120          125
178 Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr
179           130          135          140
181 Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met
182 145           150          155          160
184 Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys
185           165          170          175
187 Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala
188           180          185          190
190 Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp
191           195          200          205
193 Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys
194           210          215          220
196 Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys
197 225           230          235          240
199 Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu
200           245          250          255

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DATE: 12/09/2002

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TIME: 12:55:28

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

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202 Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys
203           260           265           270
205 Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln
206           275           280           285
208 His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly
209           290           295           300
211 Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu
212 305           310           315           320
214 Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys
215           325           330           335
217 Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn
218           340           345           350
220 Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His
221           355           360           365
223 Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro
224           370           375           380
226 Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala
227 385           390           395           400
229 Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly
230           405           410           415
232 Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr
233           420           425           430
235 Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp
236           435           440           445
238 Pro Cys Glu Val Asp Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys
239           450           455           460
241 Thr Thr Ser Leu Cys Val Ile Ser Lys
242 465           470

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245 <210> SEQ ID NO: 4

246 <211> LENGTH: 1422

247 <212> TYPE: DNA

248 <213> ORGANISM: Artificial Sequence

250 <220> FEATURE:

251 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA Nucleotide

252 Sequence

254 <400> SEQUENCE: 4

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256 aatatagaag gcagtggagg aaatgatgag cttcttgagc agaacgtgtg gaacgatgta 120
257 gacgacaagg ttgtagaagc acttggtggt cttgatgatg aactgctaac cgaacatgtg 180
258 tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa 240
259 ttacgaagat cattggcttt cggaagcaa agaaacaaga gaggtctcat gaacggtgcg 300
260 agaaatatgt ataaactgga ttgggattgt gaactggcat cacttgacgc caattggtca 360
261 acctcctgcc ctacgactt tatgccgcaa tcggtacttg gctccaacgc tcagcttttt 420
262 aagcgtttct atttttattt tgatggggcac gactctactg tacatatgcg aaacgcgatg 480
263 aagtattggt ggcagcaagg tgaagaaaaa ggcaatgagg atcagaaaaa tagattctat 540
264 gccagacgaa attattttgg atgggcaaac atggcaaaaag gaaaaacata tcgagttgga 600
265 tgctcgataa ttatgtgcgg cgacggtgaa tctgcacttt tcacttgtct ttataacgaa 660
266 aaagcccaat gcgaaaaaga aatgatattac gaaaatggaa aaccctgctg tgaggataaa 720
267 gactgtttca catatccagg atcaaaatgt ttagtacctg aaggattatg tcaagcacct 780

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DATE: 12/09/2002

PATENT APPLICATION: US/10/051,644A

TIME: 12:55:28

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

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268 tctatggttaa aggatgatgg aggaagtttc caatgtgata actcccttgt gtcagatgtc 840
269 acccgcaatt tcacttttga gcaacacaat ttttatagat ctcgtcttgc aaaagggtttt 900
270 gaatggaatg gagaaacaaa cacttcccag ccaaaggcta gtcaaataatg caaaatggag 960
271 tatgactgca tgttggaacg gtttgcacaa aactgggcaa ataattgcgt ttttgcacac 1020
272 tcggcacatt acgaaagacc gaatcagggt cagaatctct acatgagttc tttctcaaac 1080
273 cctgataccta gaagccttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140
274 ttcggtactc caattgataa cgttctgaca cccgaattgt gggatttgaa agggaaagcg 1200
275 ataggacatt acactcagat ggccctggat cgtacttacc gtcttggttg tggaatcgca 1260
276 aactgtccga agatgtcgta cgtggtttgt cactatgggc cagcaggcaa cagaaagaac 1320
277 aataaaatct atgaaatcgg ggatccttgc gaagtcgatg atgattgccg gattggaaca 1380
278 gattgtgaaa agacaacttc tttatgtgtg atctcaaaat aa 1422
281 <210> SEQ ID NO: 5
282 <211> LENGTH: 218
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence:Clustal W
288 Alignment of VAP-1, VAP-2, and Selected Other
289 Nematode VA Proteins.
291 <400> SEQUENCE: 5
292 Met Phe Ser Pro Val Ile Val Ser Val Ile Phe Thr Ile Ala Phe Cys
293 1 5 10 15
295 Asp Ala Ser Pro Ala Arg Asp Gly Phe Gly Cys Ser Asn Ser Gly Ile
296 20 25 30
298 Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg
299 35 40 45
301 Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn
302 50 55 60
304 Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln
305 65 70 75 80
307 Gln Leu Gln Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile
308 85 90 95
310 Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe
311 100 105 110
313 Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser
314 115 120 125
316 Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly
317 130 135 140
319 Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu
320 145 150 155 160
322 Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile
323 165 170 175
325 Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly
326 180 185 190
328 Gln Ala Cys Lys Thr Gly Ala Asp Cys Ser Thr Tyr Lys Asn Ser Gly
329 195 200 205
331 Cys Glu Asp Gly Leu Cys Thr Lys Gly Pro
332 210 215
335 <210> SEQ ID NO: 6

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/051,644A

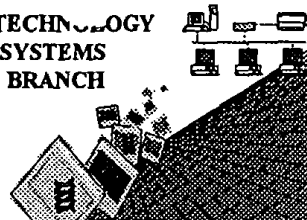
DATE: 12/09/2002

TIME: 12:55:29

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\12092002\J051644A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date



0590
1126

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/051,644A
Source: 01P2
Date Processed by STIC: 12/9/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002